

Serial Number: 09/807,902CRF Processing Date: 1/17/95

Edited by: \_\_\_\_\_

Verified by: \_\_\_\_\_ (STIC sta

**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

## RAW SEQUENCE LISTING

DATE: 07/17/2001

PATENT APPLICATION: US/09/857,902

TIME: 17:04:40

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\07172001\I857902.raw

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5 <110> APPLICANT: Sedlacek, et al.
7 <120> TITLE OF INVENTION: Spermatogenesis Protein
9 <130> FILE REFERENCE: 4121-125
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/857,902
C--> 12 <141> CURRENT FILING DATE: 2001-06-08
14 <150> PRIOR APPLICATION NUMBER: DE 198 56 882.7
15 <151> PRIOR FILING DATE: 1998-12-10
17 <160> NUMBER OF SEQ ID NOS: 7
19 <170> SOFTWARE: PatentIn Ver. 2.1.
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1618
25 <212> TYPE: DNA
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30 <222> LOCATION: (113)..(1087)
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39                                     Met
40                                     1
42 gcg cag tac aag ggc acc atg cgc gag gca ggc cgt gcc atg cac ctc      163
43 Ala Gln Tyr Lys Gly Thr Met Arg Glu Ala Gly Arg Ala Met His Leu
44             5             10             15
46 ctc aag aag cgc gaa agg cag cgg gag cag atg gag gtg ctg aag cag      211
47 Leu Lys Lys Arg Glu Arg Gln Arg Glu Gln Met Glu Val Leu Lys Gln
48             20             25             30
50 cgc atc gcc gag gag acc atc ctc aag tcg cag gtg gac aag agg ttc      259
51 Arg Ile Ala Glu Glu Thr Ile Leu Lys Ser Gln Val Asp Lys Arg Phe
52             35             40             45
54 tcg gcg cat tac gac gcc gtg gag gcc gag ctg aag tcc agc acg gtg      307
55 Ser Ala His Tyr Asp Ala Val Glu Ala Glu Leu Lys Ser Ser Thr Val
56 50             55             60             65
58 ggc ctg gtg acc ctg aac gac atg aag gcc cgg cag gag gcc ctg gtc      355
59 Gly Leu Val Thr Leu Asn Asp Met Lys Ala Arg Gln Glu Ala Leu Val
60             70             75             80
62 agg gag cgc gag cgg cag ctg gcc aag cgc cag cac ctg gag gag cag      403
63 Arg Glu Arg Glu Arg Gln Leu Ala Lys Arg Gln His Leu Glu Glu Gln
64             85             90             95
68 cgg ctg cag cag gag cgg cag cgg gag cag gag cag cgg cgc gag cgc      451
69 Arg Leu Gln Gln Glu Arg Gln Arg Glu Gln Glu Gln Arg Arg Glu Arg
70             100            105            110
72 aag cgt aag atc tcc tgc ctg tcc ttt gca cta gac gac ctc gat gac      499
73 Lys Arg Lys Ile Ser Cys Leu Ser Phe Ala Leu Asp Asp Leu Asp Asp
74             115            120            125
76 cag gcc gac gcg gcc gag gcc agg cgc gcc gga aac ctg ggc aag aac      547
77 Gln Ala Asp Ala Ala Glu Ala Arg Arg Ala Gly Asn Leu Gly Lys Asn

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DATE: 07/17/2001

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82          150          155          160
84 gag aac cgg ctg cga gag gag ctg cgc caa gag tgg gag gcg cag cgc      643
85 Glu Asn Arg Leu Arg Glu Glu Leu Arg Gln Glu Trp Glu Ala Gln Arg
86          165          170          175
88 gag aaa gtg aag gac gag gag atg gag gtc acc ttc agc tac tgg gac      691
89 Glu Lys Val Lys Asp Glu Glu Met Glu Val Thr Phe Ser Tyr Trp Asp
90          180          185          190
92 ggc tcg ggc cac cgg cgc acg gtg cgg gtg cgc aag ggc aac acg gtg      739
93 Gly Ser Gly His Arg Arg Thr Val Arg Val Arg Lys Gly Asn Thr Val
94          195          200          205
96 cag cag ttc ctg aag aag gcg ctg cag ggg ctg cgc aag gac ttc ctg      787
97 Gln Gln Phe Leu Lys Lys Ala Leu Gln Gly Leu Arg Lys Asp Phe Leu
98 210          215          220          225
100 gag ctg cgc tcc gcc ggc gtg gag cag ctg atg ttc atc aag gag gac      835
101 Glu Leu Arg Ser Ala Gly Val Glu Gln Leu Met Phe Ile Lys Glu Asp
102          230          235          240
104 ctg atc ctg ccg cac tac cac acc ttc tac gac ttc atc atc gcc agg      883
105 Leu Ile Leu Pro His Tyr His Thr Phe Tyr Asp Phe Ile Ile Ala Arg
106          245          250          255
108 gcg agg ggc aag agc ggg ccg ctg ttc agc ttc gat gtg cac gat gac      931
109 Ala Arg Gly Lys Ser Gly Pro Leu Phe Ser Phe Asp Val His Asp Asp
110          260          265          270
112 gtg cgc ctg ctg agc gac gcc acc atg gag aag gac gag tcg cac gcg      979
113 Val Arg Leu Leu Ser Asp Ala Thr Met Glu Lys Asp Glu Ser His Ala
114          275          280          285
116 ggc aag gtg gtg ctg cgc agc tgg tac gag aag aac aag cac atc ttc      1027
117 Gly Lys Val Val Leu Arg Ser Trp Tyr Glu Lys Asn Lys His Ile Phe
118 290          295          300          305
120 ccc gcc agc cgc tgg gag gcc tat gac ccc gag aag aag tgg gac aag      1075
121 Pro Ala Ser Arg Trp Glu Ala Tyr Asp Pro Glu Lys Lys Trp Asp Lys
122          310          315          320
124 tac acc atc cgc/taacacccgc ctgccagagc ggaaaccggg ggtgggggga      1127
125 Tyr Thr Ile Arg
126          325
128 gacactcatt tctaggcccc atcaccagtc acttgatttc gtgaccttga tttcttcccc      1187
130 caaatttaaat aaagacagag ggttctcatg attcacattg gttgtgctat tgctgatgtt      1247
132 atgcttttgtt tgcttggttg gtcttttctg agtatttttag tgttgccacc tggatttgct      1307
134 gcattgctct gctgagctgt attgaaacca tgactgggcc cactgtcaga cagaaattag      1367
136 aataggaggc acatttttta cctggtggtt atgagcatgg acttgggggc cacagtgact      1427
138 gagtttgatt cccgacacag cctcctcctt gctgtgtagt tttgggtaag cttattaaac      1487
140 ccccatgcct cagtttggtc acctgtaaaa ggaaataaca agagcactta ctttataaga      1547
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148 <210> SEQ ID NO: 2
149 <211> LENGTH: 325
150 <212> TYPE: PRT

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151 &lt;213&gt; ORGANISM: Human

153 &lt;400&gt; SEQUENCE: 2

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160           20           25           30
162 Gln Arg Ile Ala Glu Glu Thr Ile Leu Lys Ser Gln Val Asp Lys Arg
163           35           40           45
165 Phe Ser Ala His Tyr Asp Ala Val Glu Ala Glu Leu Lys Ser Ser Thr
166           50           55           60
168 Val Gly Leu Val Thr Leu Asn Asp Met Lys Ala Arg Gln Glu Ala Leu
169   65           70           75           80
171 Val Arg Glu Arg Glu Arg Gln Leu Ala Lys Arg Gln His Leu Glu Glu
172           85           90           95
174 Gln Arg Leu Gln Gln Glu Arg Gln Arg Glu Gln Glu Gln Arg Arg Glu
175           100          105          110
177 Arg Lys Arg Lys Ile Ser Cys Leu Ser Phe Ala Leu Asp Asp Leu Asp
178           115          120          125
180 Asp Gln Ala Asp Ala Ala Glu Ala Arg Arg Ala Gly Asn Leu Gly Lys
181           130          135          140
183 Asn Pro Asp Val Asp Thr Ser Phe Leu Pro Asp Arg Asp Arg Glu Glu
184 145          150          155          160
186 Glu Glu Asn Arg Leu Arg Glu Glu Leu Arg Gln Glu Trp Glu Ala Gln
187           165          170          175
189 Arg Glu Lys Val Lys Asp Glu Glu Met Glu Val Thr Phe Ser Tyr Trp
190           180          185          190
192 Asp Gly Ser Gly His Arg Arg Thr Val Arg Val Arg Lys Gly Asn Thr
193           195          200          205
195 Val Gln Gln Phe Leu Lys Lys Ala Leu Gln Gly Leu Arg Lys Asp Phe
196           210          215          220
198 Leu Glu Leu Arg Ser Ala Gly Val Glu Gln Leu Met Phe Ile Lys Glu
199 225          230          235          240
201 Asp Leu Ile Leu Pro His Tyr His Thr Phe Tyr Asp Phe Ile Ile Ala
202           245          250          255
204 Arg Ala Arg Gly Lys Ser Gly Pro Leu Phe Ser Phe Asp Val His Asp
205           260          265          270
207 Asp Val Arg Leu Leu Ser Asp Ala Thr Met Glu Lys Asp Glu Ser His
208           275          280          285
210 Ala Gly Lys Val Val Leu Arg Ser Trp Tyr Glu Lys Asn Lys His Ile
211           290          295          300
213 Phe Pro Ala Ser Arg Trp Glu Ala Tyr Asp Pro Glu Lys Lys Trp Asp
214 305          310          315          320
216 Lys Tyr Thr Ile Arg
217           325

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220 &lt;210&gt; SEQ ID NO: 3

221 &lt;211&gt; LENGTH: 2875

222 &lt;212&gt; TYPE: DNA

223 &lt;213&gt; ORGANISM: Human

225 &lt;400&gt; SEQUENCE: 3

## RAW SEQUENCE LISTING

DATE: 07/17/2001

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230	gcatgttaga	ggctcacagt	aaagacactg	ctacacttta	actcagtgtc	ccatggttat	120
232	tagagcttag	aaccgggg	aaactgctgt	atagaagagg	tcaaacaagc	tgagtgcagg	180
234	ttttgtcacg	aaactggggg	gcgagtaggg	ttctattatc	aaagaatggt	tgtgttgggg	240
236	ccataagaaa	gaattacagg	cagtgggtgcg	caggtaatgt	tcacgagacg	ccacagcggg	300
238	gtagcatcag	aggcgggagg	aggagggttg	gagagcaggg	ccgtgttgca	aggctctctg	360
240	ggtggccaca	gcagcttgcg	ctgcgcccac	attgcttctg	cgtgtttaca	gctgggcacg	420
242	agaaggtca	gcacgcacgc	acagcagggtg	ggggcccgcc	ctgccacag	cgtgaaaaca	480
244	ggagcccccg	ccagccacgg	ctgggcaggg	ccagaagcgc	ctcctccagg	atcctccccg	540
246	cgctggcccc	ccccacagga	gcaccgcccc	taccaggagc	ccggagctct	tcccaggggc	600
248	cgctcccccg	ccagggggcg	atccacctcc	acttctctgt	tccgcagccg	ccctaccagg	660
250	agcctggcac	tctcctcagg	gcccgcctcc	ccgccagggg	gcgcaccgcc	tccacttcct	720
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254	tggaggtcag	ctcccgcgtg	tctccgctcg	acaggggtgt	tgggcaggta	aggggtccgct	840
256	cagtagccca	accctctctg	tatgcagctc	cccaaattca	gcgctgcgct	caggcatggc	900
258	agccaccctg	tacgtggggc	cgttcgcatt	tgcattttatt	gaggtcaa	aaaatgctgg	960
260	aaattgggtgc	ctggtgacac	tgtaggttg	gtggttacct	tagcaggtcg	gcccagcccc	1020
262	tgaacgcttc	catcactgcc	gaaagccctg	tgaggaggcg	cagagctgag	cattccccgc	1080
264	cgttgcgtgg	gccccctct	acctgccgcg	tttttctct	ttgctgcaga	gcccacggg	1140
266	taggcgcggg	ccatggcgca	gtacaagggc	accatgcgcg	aggcaggccg	tgccatgcac	1200
268	ctcctcaaga	agcgcgaaag	gcagcgggag	cagatggagg	tgctgaagca	gcgcacgcc	1260
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292	agggcgaggg	gcaagagcgg	gccgctcttc	agcttcgatg	tgacgatga	cgtgcgcctg	1980
294	ctcagcgacg	ccaccatgga	gaaggacgag	tcgcacgcgg	gcaaggtggt	gctgcgcagc	2040
296	tggtaggaga	agaacaagca	catcttcccc	gccagccgct	gggaggccta	tgaccccgag	2100
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310	agtgactgag	tttgattccc	gacacagcct	cctccttgct	gtgtagtttt	gggtaagctt	2520
312	attaaacccc	catgcctcag	tttggtcacc	tgtaaaagga	aataacaaga	gcacttactt	2580
314	tataagattg	atgtgagtat	taagtgaatt	aatatttgta	aaacgcttag	ctcttaataa	2640
316	atgtttctgt	tggttatttt	atggttttgg	ttaattttat	taaaggactg	caatgacctg	2700
318	gttcagaact	atttgagggc	aaaggtggac	gtgcccata	ctgggtcccag	gatcagcagt	2760
320	tgccagcagg	agggggctag	caaaggttgg	ggagcagccc	ccctctagtg	ggcttttagct	2820
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/857,902

DATE: 07/17/2001

TIME: 17:04:41

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Output Set: N:\CRF3\07172001\I857902.raw

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328 <212> TYPE: DNA
329 <213> ORGANISM: Mouse
331 <220> FEATURE:
332 <221> NAME/KEY: CDS
333 <222> LOCATION: (137)..(1138) ✓
335 <400> SEQUENCE: 4
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340 gaactgacat cagaccagaaggctaccag aaacagggac tgggcaggcc aaaaagcctt      120
342 gcgctgaact gcaggc 'atg gcg cag tac aaa ggc acc atg cgg gaa gct      169
343           Met Ala Gln Tyr Lys Gly Thr Met Arg Glu Ala
344           1           5           10
346 ggc cgg gcc atg cac ctg atc aag aag cgt gag aag cag aag gag cag      217
347 Gly Arg Ala Met His Leu Ile Lys Lys Arg Glu Lys Gln Lys Glu Gln
348           15           20           25
350 atg gag gtg ctg aag cag cgc atc gca gag gag acc atc atg aag tca      265
351 Met Glu Val Leu Lys Gln Arg Ile Ala Glu Glu Thr Ile Met Lys Ser
352           30           35           40
354 aaa gtg gac aag aag ttc tcg gca cac tac gac gcc gtg gag gcc gag      313
355 Lys Val Asp Lys Lys Phe Ser Ala His Tyr Asp Ala Val Glu Ala Glu
356           45           50           55
358 ctg aag tcc agt acg gtg ggc ctg gtg acc ctg aat gac atg aag gcc      361
359 Leu Lys Ser Ser Thr Val Gly Leu Val Thr Leu Asn Asp Met Lys Ala
360 60           65           70           75
362 aag cag gag gcc ctg ctg agg gag cgg gag atg cag ctg gcc aag agg      409
363 Lys Gln Glu Ala Leu Leu Arg Glu Arg Glu Met Gln Leu Ala Lys Arg
364           80           85           90
366 gag cag ctg gag caa cgc cgg ata cag ctg gag atg ctg cgc gag aag      457
367 Glu Gln Leu Glu Gln Arg Arg Ile Gln Leu Glu Met Leu Arg Glu Lys
368           95           100          105
370 gag cga agg cga gag cgc aag cgc aag atc tcc aac ctg tct ttc acg      505
371 Glu Arg Arg Arg Glu Arg Lys Arg Lys Ile Ser Asn Leu Ser Phe Thr
372           110          115          120
374 ttg gac gag gaa gaa ggt gac caa gag gac agc cgc caa gcc gag agt      553
375 Leu Asp Glu Glu Glu Gly Asp Gln Glu Asp Ser Arg Gln Ala Glu Ser
376           125          130          135
378 gcc gag gcc cac agt gct gga gcc aag aag aac ttg ggc aag aat ccc      601
379 Ala Glu Ala His Ser Ala Gly Ala Lys Lys Asn Leu Gly Lys Asn Pro
380 140          145          150          155
382 gat gtg gac acg agc ttc ctg ccc gac cgc gag cgc gag gag gag gag      649
383 Asp Val Asp Thr Ser Phe Leu Pro Asp Arg Glu Arg Glu Glu Glu Glu
384           160          165          170
386 aac cgg ttg cgc gag gaa ctg cgg cag gag tgg gag gcg aag cgc gag      697
387 Asn Arg Leu Arg Glu Glu Leu Arg Gln Glu Trp Glu Ala Lys Arg Glu
388           175          180          185
390 aag gtg aag ggc gag gag gtg gag atc acc ttc agc tac tgg gat ggc      745
391 Lys Val Lys Gly Glu Glu Val Glu Ile Thr Phe Ser Tyr Trp Asp Gly
392           190          195          200
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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/857,902

DATE: 07/17/2001

TIME: 17:04:42

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date